<!--StartFragment-->RESULT 1
Q12621_HUMGT
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ID   Q12621_HUMGT   PRELIMINARY;   PRT;   525 AA.
AC   Q12621;
DT   01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 31.
DE   Cellulase (EC 3.2.1.91).
GN   Name=cbh-1;
OS   Humicola grisea var. thermoidea.
OC   Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX   NCBI_TaxID=5528;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=IFO9854;
RA   Takashima S., Nakamura A., Hidaka M., Masaki H., Uozumi T.;
RT   "Cloning, sequencing, and expression of the cellulase genes of
RT   Humicola grisea var. thermoidea.";
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: The biological conversion of cellulose to glucose
CC       generally requires three types of hydrolytic enzymes: (1)
CC       Endoglucanases which cut internal beta-1,4-glucosidic bonds; (2)
CC       Exocellobiohydrolases that cut the dissaccharide cellobiose from
CC       the nonreducing end of the cellulose polymer chain; (3) Beta-1,4-
CC       glucosidases which hydrolyze the cellobiose and other short cello-
CC       oligosaccharides to glucose (By similarity).
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
CC       in cellulose and cellotetraose, releasing cellobiose from the non-
CC       reducing ends of the chains.
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; D63515; BAA09785.1; -; Genomic_DNA.
DR   HSSP; Q09431; 1GPI.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0016162; F:cellulose 1,4-beta-cellobiosidase activity; IEA.
DR   GO; GO:0030248; F:cellulose binding; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   GO; GO:0030245; P:cellulose catabolism; IEA.
DR   GO; GO:0000272; P:polysaccharide catabolism; IEA.
DR   InterPro; IPR000254; CBD_fun.
DR   InterPro; IPR001722; Glyco_hydro_7.
DR   Pfam; PF00734; CBM_1; 1.
DR   Pfam; PF00840; Glyco_hydro_7; 1.
DR   PRINTS; PR00734; GLHYDRLASE7.
DR   ProDom; PD001821; CBD_fungal; 1.
DR   ProDom; PD186135; Glyco_hydro_7; 1.
DR   SMART; SM00236; fCBD; 1.
DR   PROSITE; PS00562; CBD_FUNGAL; 1.
KW   Carbohydrate metabolism; Cellulose degradation; Glycosidase;
KW   Hydrolase; Polysaccharide degradation.
SQ   SEQUENCE   525 AA;   55722 MW;   A2E6E5F40F6D3BB0 CRC64;
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   Query Match             99.8%;   Score 2799;   DB 2;   Length 525;
   Best Local Similarity   99.8%;   Pred. No. 1.7e-184;
   Matches   506;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;


Qy       1 QQACSLTTERHPSLSWKKCTAGGQCQTVQASITLDSNWRWTHQVSGSTNCYTGNKWDTSI 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19 QQACSLTTERHPSLSWKKCTAGGQCQTVQASITLDSNWRWTHQVSGSTNCYTGNKWDTSI 78
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Qy        61  CTDAKSCAQNCCVDGADYTSTYGITTNGDSLSLKFVTKGQHSTNVGSRTYLMDGEDKYQT  120
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Db        79  CTDAKSCAQNCCVDGADYTSTYGITTNGDSLSLKFVTKGQYSTNVGSRTYLMDGEDKYQT  138

Qy       121  FELLGNEFTFDVDVSNIGCGLNGALYFVSMDADGGLSRYPGNKAGAKYGTGYCDAQCPRD  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       139  FELLGNEFTFDVDVSNIGCGLNGALYFVSMDADGGLSRYPGNKAGAKYGTGYCDAQCPRD  198

Qy       181  IKFINGEANIEGWTGSTNDPNAGAGRYGTCCSEMDIWEANNMATAFTPHPCTIIGQSRCE  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       199  IKFINGEANIEGWTGSTNDPNAGAGRYGTCCSEMDIWEANNMATAFTPHPCTIIGQSRCE  258

Qy       241  GDSCGGTYSNERYAGVCDPDGCDFNSYRQGNKTFYGKGMTVDTTKKITVVTQFLKDANGD  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       259  GDSCGGTYSNERYAGVCDPDGCDFNSYRQGNKTFYGKGMTVDTTKKITVVTQFLKDANGD  318

Qy       301  LGEIKRFYVQDGKIIPNSESTIPGVEGNSITQDWCDRQKVAFGDIDDFNRKGGMKQMGKA  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       319  LGEIKRFYVQDGKIIPNSESTIPGVEGNSITQDWCDRQKVAFGDIDDFNRKGGMKQMGKA  378

Qy       361  LAGPMVLVMSIWDDHASNMLWLDSTFPVDAAGKPGAERGACPTTSGVPAEVEAEAPNSNV  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       379  LAGPMVLVMSIWDDHASNMLWLDSTFPVDAAGKPGAERGACPTTSGVPAEVEAEAPNSNV  438

Qy       421  VFSNIRFGPIGSTVAGLPGAGNGGNNGGNPPPPTTTTSSAPATTTTASAGPKAGRWQQCG  480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       439  VFSNIRFGPIGSTVAGLPGAGNGGNNGGNPPPPTTTTSSAPATTTTASAGPKAGRWQQCG  498

Qy       481  GIGFTGPTQCEEPYTCTKLNDWYSQCL  507
              |||||||||||||||||||||||||||
Db       499  GIGFTGPTQCEEPYTCTKLNDWYSQCL  525


<!--EndFragment-->
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